

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/533,176
Source: PCP/10
Date Processed by STIC: 5/12/05

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PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/533,176

DATE: 05/12/2005
TIME: 08:25:16

Input Set : D:\1392-10-20-PCT.ST25.txt
Output Set: N:\CRF4\05122005\J533176.raw

3 <110> APPLICANT: Syngenta Participations, AG
4 Cooper, Bret
6 <120> TITLE OF INVENTION: STRESS-RELATED POLYPEPTIDES AND USES THEREFOR
8 <130> FILE REFERENCE: 1392-10-20 PCT
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/533,176
C--> 10 <141> CURRENT FILING DATE: 2005-04-29
10 <150> PRIOR APPLICATION NUMBER: US 60/436,564
11 <151> PRIOR FILING DATE: 2002-12-26
13 <160> NUMBER OF SEQ ID NOS: 174
15 <170> SOFTWARE: PatentIn version 3.2
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1383
19 <212> TYPE: DNA
20 <213> ORGANISM: Oryza sativa
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (1)..(1383)
27 <400> SEQUENCE: 1
28 gct tcc ttt cgg act gtt ggt gct aaa atc act cag gaa act ggt gat 48
29 Ala Ser Phe Arg Thr Val Gly Ala Lys Ile Thr Gln Glu Thr Gly Asp
30 1 5 10 15
32 ttc ttt gtt agc gat gca gag ggt gac cca gac aaa cca act gat ggt 96
33 Phe Phe Val Ser Asp Ala Glu Gly Asp Pro Asp Lys Pro Thr Asp Gly
34 20 25 30
36 ttt tcc tct att gat gag gct ata ggc gca ttg cat gaa gga aag ttt 144
37 Phe Ser Ser Ile Asp Glu Ala Ile Gly Ala Leu His Glu Gly Lys Phe
38 35 40 45
40 gtt att gct gta gat gat gaa agc ggt gat aat gaa ggg gat ctt gtc 192
41 Val Ile Ala Val Asp Asp Glu Ser Gly Asp Asn Glu Gly Asp Leu Val
42 50 55 60
44 atg gca gct acg ctg gca gac cca gaa tct att gca ttc atg atc agg 240
45 Met Ala Ala Thr Leu Ala Asp Pro Glu Ser Ile Ala Phe Met Ile Arg
46 65 70 75 80
48 aat ggt tct ggg atc atc tca gtg ggc atg aag gaa gag gac tta aca 288
49 Asn Gly Ser Gly Ile Ile Ser Val Gly Met Lys Glu Glu Asp Leu Thr
50 85 90 95
52 aga ttg atg att cct atg atg tct cca att gca gaa att gag gat att 336
53 Arg Leu Met Ile Pro Met Met Ser Pro Ile Ala Glu Ile Glu Asp Ile
54 100 105 110
56 tca gct gct tcc aca gta aca gtg gat gcc aga gtg ggc ata tca 384
57 Ser Ala Ala Ala Ser Thr Val Thr Val Asp Ala Arg Val Gly Ile Ser
58 115 120 125
60 acc ggc gtc tcg gct gca gat agg gca aaa acg att ttt act cta gcc 432

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61	Thr	Gly	Val	Ser	Ala	Ala	Asp	Arg	Ala	Lys	Thr	Ile	Phe	Thr	Leu	Ala	
62	130				135					140							
64	tcc	cct	gat	tct	aag	cca	act	gac	ctc	aga	aga	cca	ggc	cat	ata	ttc	480
65	Ser	Pro	Asp	Ser	Lys	Pro	Thr	Asp	Leu	Arg	Arg	Pro	Gly	His	Ile	Phe	
66	145				150					155					160		
68	cct	cta	aaa	tac	cga	aac	ggt	ggt	gtg	cta	aaa	aga	gct	gga	cat	act	528
69	Pro	Leu	Lys	Tyr	Arg	Asn	Gly	Gly	Val	Leu	Lys	Arg	Ala	Gly	His	Thr	
70		165				170				175							
72	gag	gca	tcc	gtc	gat	ctt	gtc	gcg	ttg	gct	ggc	ttg	cgc	cct	gtg	tct	576
73	Glu	Ala	Ser	Val	Asp	Leu	Val	Ala	Leu	Ala	Gly	Leu	Arg	Pro	Val	Ser	
74		180			185					190							
76	gtc	ctg	tca	acc	gtc	atc	aac	cca	gtg	gat	ggg	tca	atg	gca	gga	atg	624
77	Val	Leu	Ser	Thr	Val	Ile	Asn	Pro	Val	Asp	Gly	Ser	Met	Ala	Gly	Met	
78		195			200				205								
80	cca	gtg	ctg	aaa	cag	atg	gct	ttg	gag	cat	gat	atc	cca	att	gtt	tca	672
81	Pro	Val	Leu	Lys	Gln	Met	Ala	Leu	Glu	His	Asp	Ile	Pro	Ile	Val	Ser	
82		210			215				220								
84	atc	gct	gat	ctc	atc	cgg	tat	aga	agg	aag	agg	gag	aag	ctg	gtg	gaa	720
85	Ile	Ala	Asp	Leu	Ile	Arg	Tyr	Arg	Arg	Lys	Arg	Glu	Lys	Leu	Val	Glu	
86	225		230			235				240							
88	ctg	att	gct	gta	tct	cgt	ttg	ccg	acg	aaa	ttg	ggc	ctt	ttc	cga	gct	768
89	Leu	Ile	Ala	Val	Ser	Arg	Leu	Pro	Thr	Lys	Trp	Gly	Leu	Phe	Arg	Ala	
90		245			250				255								
92	tac	tgc	tac	caa	tcc	aag	ctt	gat	gga	acc	gag	cac	att	gct	gtt	gca	816
93	Tyr	Cys	Tyr	Gln	Ser	Lys	Leu	Asp	Gly	Thr	Glu	His	Ile	Ala	Val	Ala	
94		260			265				270								
96	aag	ggc	gac	atc	ggc	gac	ggc	gag	gac	gtc	ttg	gtg	agg	gtc	cat	tcc	864
97	Lys	Gly	Asp	Ile	Gly	Asp	Gly	Glu	Asp	Val	Leu	Val	Arg	Val	His	Ser	
98		275			280				285								
100	gag	tgc	ctg	acc	ggc	gac	atc	ctc	ggc	tcc	gcc	cgc	tgc	gac	tgc	ggc	912
101	Glu	Cys	Leu	Thr	Gly	Asp	Ile	Leu	Gly	Ser	Ala	Arg	Cys	Asp	Cys	Gly	
102		290			295				300								
104	aac	cag	ctg	gac	ctg	ggc	atg	cag	ctc	atc	gac	aag	gcc	ggc	ggc	960	
105	Asn	Gln	Leu	Asp	Leu	Ala	Met	Gln	Leu	Ile	Asp	Lys	Ala	Gly	Arg	Gly	
106	305		310			315				320							
108	gtc	ctc	gtc	tac	ctc	cgc	ggc	cac	gag	ggc	cgc	ggc	atc	ggc	ctc	ggc	1008
109	Val	Leu	Val	Tyr	Leu	Arg	Gly	His	Glu	Gly	Arg	Gly	Ile	Gly	Leu	Gly	
110		325			330				335								
112	cag	aag	ctc	cgc	tac	aac	ctc	cag	gac	ggc	cac	gac	acc	gtc		1056	
113	Gln	Lys	Leu	Arg	Ala	Tyr	Asn	Leu	Gln	Asp	Asp	Gly	His	Asp	Thr	Val	
114		340			345				350								
116	cag	gcc	aac	gtc	gag	ctc	ggc	ctc	gcc	gac	tcc	cgc	gag	tac	ggc	1104	
117	Gln	Ala	Asn	Val	Glu	Leu	Gly	Leu	Ala	Val	Asp	Ser	Arg	Glu	Tyr	Gly	
118		355			360				365								
120	atc	ggc	gcc	cag	att	ctg	cgg	gac	atg	ggg	gtg	cgc	acg	atg	cg	ctg	1152
121	Ile	Gly	Ala	Gln	Ile	Leu	Arg	Asp	Met	Gly	Val	Arg	Thr	Met	Arg	Leu	
122		370			375				380								
124	atg	acg	aac	aac	ccg	gca	aag	ttc	gtc	ggg	ctc	aag	ggc	tac	ggg	ctc	1200
125	Met	Thr	Asn	Asn	Pro	Ala	Lys	Phe	Val	Gly	Leu	Lys	Gly	Tyr	Gly	Leu	

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126	385	390	395	400	
128	gcc gtc gtc ggc agg gtt ccg gtg atc tcc ccc atc acc aag gag aac				1248
129	Ala Val Val Gly Arg Val Pro Val Ile Ser Pro Ile Thr Lys Glu Asn				
130	405	410	415		
132	cag agg tac ctc gag acg aag cgc acc aag atg ggc cat gtc tac ggc				1296
133	Gln Arg Tyr Leu Glu Thr Lys Arg Thr Lys Met Gly His Val Tyr Gly				
134	420	425	430		
136	tcc gac ctc ccc ggc aac gtc ccg gag gaa ttc ctc aac ccg gac gac				1344
137	Ser Asp Leu Pro Gly Asn Val Pro Glu Glu Phe Leu Asn Pro Asp Asp				
138	435	440	445		
140	atc gcc gga gac caa gac gaa gac gac acc cac aac tga				1383
141	Ile Ala Gly Asp Gln Asp Glu Asp Asp Thr His Asn				
142	450	455	460		
145	<210> SEQ ID NO: 2				
146	<211> LENGTH: 460				
147	<212> TYPE: PRT				
148	<213> ORGANISM: Oryza sativa				
150	<400> SEQUENCE: 2				
152	Ala Ser Phe Arg Thr Val Gly Ala Lys Ile Thr Gln Glu Thr Gly Asp				
153	1	5	10	15	
156	Phe Phe Val Ser Asp Ala Glu Gly Asp Pro Asp Lys Pro Thr Asp Gly				
157	20	25	30		
160	Phe Ser Ser Ile Asp Glu Ala Ile Gly Ala Leu His Glu Gly Lys Phe				
161	35	40	45		
164	Val Ile Ala Val Asp Asp Glu Ser Gly Asp Asn Glu Gly Asp Leu Val				
165	50	55	60		
168	Met Ala Ala Thr Leu Ala Asp Pro Glu Ser Ile Ala Phe Met Ile Arg				
169	65	70	75	80	
172	Asn Gly Ser Gly Ile Ile Ser Val Gly Met Lys Glu Glu Asp Leu Thr				
173	85	90	95		
176	Arg Leu Met Ile Pro Met Met Ser Pro Ile Ala Glu Ile Glu Asp Ile				
177	100	105	110		
180	Ser Ala Ala Ala Ser Thr Val Thr Val Asp Ala Arg Val Gly Ile Ser				
181	115	120	125		
184	Thr Gly Val Ser Ala Ala Asp Arg Ala Lys Thr Ile Phe Thr Leu Ala				
185	130	135	140		
188	Ser Pro Asp Ser Lys Pro Thr Asp Leu Arg Arg Pro Gly His Ile Phe				
189	145	150	155	160	
192	Pro Leu Lys Tyr Arg Asn Gly Gly Val Leu Lys Arg Ala Gly His Thr				
193	165	170	175		
196	Glu Ala Ser Val Asp Leu Val Ala Leu Ala Gly Leu Arg Pro Val Ser				
197	180	185	190		
200	Val Leu Ser Thr Val Ile Asn Pro Val Asp Gly Ser Met Ala Gly Met				
201	195	200	205		
204	Pro Val Leu Lys Gln Met Ala Leu Glu His Asp Ile Pro Ile Val Ser				
205	210	215	220		
208	Ile Ala Asp Leu Ile Arg Tyr Arg Arg Lys Arg Glu Lys Leu Val Glu				
209	225	230	235	240	
212	Leu Ile Ala Val Ser Arg Leu Pro Thr Lys Trp Gly Leu Phe Arg Ala				

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213	245	250	255	
216	Tyr Cys Tyr Gln Ser Lys Leu Asp Gly Thr Glu His Ile Ala Val Ala			
217	260	265	270	
220	Lys Gly Asp Ile Gly Asp Gly Glu Asp Val Leu Val Arg Val His Ser			
221	275	280	285	
224	Glu Cys Leu Thr Gly Asp Ile Leu Gly Ser Ala Arg Cys Asp Cys Gly			
225	290	295	300	
228	Asn Gln Leu Asp Leu Ala Met Gln Leu Ile Asp Lys Ala Gly Arg Gly			
229	305	310	315	320
232	Val Leu Val Tyr Leu Arg Gly His Glu Gly Arg Gly Ile Gly Leu Gly			
233	325	330	335	
236	Gln Lys Leu Arg Ala Tyr Asn Leu Gln Asp Asp Gly His Asp Thr Val			
237	340	345	350	
240	Gln Ala Asn Val Glu Leu Gly Leu Ala Val Asp Ser Arg Glu Tyr Gly			
241	355	360	365	
244	Ile Gly Ala Gln Ile Leu Arg Asp Met Gly Val Arg Thr Met Arg Leu			
245	370	375	380	
248	Met Thr Asn Asn Pro Ala Lys Phe Val Gly Leu Lys Gly Tyr Gly Leu			
249	385	390	395	400
252	Ala Val Val Gly Arg Val Pro Val Ile Ser Pro Ile Thr Lys Glu Asn			
253	405	410	415	
256	Gln Arg Tyr Leu Glu Thr Lys Arg Thr Lys Met Gly His Val Tyr Gly			
257	420	425	430	
260	Ser Asp Leu Pro Gly Asn Val Pro Glu Glu Phe Leu Asn Pro Asp Asp			
261	435	440	445	
264	Ile Ala Gly Asp Gln Asp Glu Asp Asp Thr His Asn			
265	450	455	460	
268	<210> SEQ ID NO: 3			
269	<211> LENGTH: 267			
270	<212> TYPE: DNA			
271	<213> ORGANISM: Oryza sativa			
274	<220> FEATURE:			
275	<221> NAME/KEY: CDS			
276	<222> LOCATION: (1)..(267)			
278	<400> SEQUENCE: 3			
279	gga acà aac cct ggc ttc aga gtt gga gag atc agg ctc tcc aac agg		48	
280	Gly Thr Asn Pro Gly Phe Arg Val Gly Glu Ile Arg Leu Ser Asn Arg			
281	1 5 10 15			
283	gat att tat ttc ggc aca tta ttg ggg aac aca cca gag ggt tca ggg		96	
284	Asp Ile Tyr Phe Gly Thr Leu Leu Gly Asn Thr Pro Glu Gly Ser Gly			
285	20 25 30			
287	agg tat gtc tgg tca gat ggt tgc act tac gat ggt gag tgg agg aga		144	
288	Arg Tyr Val Trp Ser Asp Gly Cys Thr Tyr Asp Gly Glu Trp Arg Arg			
289	35 40 45			
291	ggg atg agg cat ggg caa gga aag aca atg tgg cca tct gga gcc acc		192	
292	Gly Met Arg His Gly Gln Gly Lys Thr Met Trp Pro Ser Gly Ala Thr			
293	50 55 60			
295	tac gag ggt gag tac tct ggt ggc tac att tat ggt gaa ggc aca tat		240	
296	Tyr Glu Gly Glu Tyr Ser Gly Gly Tyr Ile Tyr Gly Glu Gly Thr Tyr			

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297	65	70	75	80													
299	acc	ggg	tct	gac	aac	atc	gtc	tac	aag	267							
300	Thr	Gly	Ser	Asp	Asn	Ile	Val	Tyr	Lys								
301										85							
304	<210>	SEQ	ID	NO:	4												
305	<211>	LENGTH:	89														
306	<212>	TYPE:	PRT														
307	<213>	ORGANISM:	Oryza sativa														
309	<400>	SEQUENCE:	4														
311	Gly	Thr	Asn	Pro	Gly	Phe	Arg	Val	Gly	Ile	Arg	Leu	Ser	Asn	Arg		
312	1									5	10	15					
315	Asp	Ile	Tyr	Phe	Gly	Thr	Leu	Leu	Gly	Asn	Thr	Pro	Glu	Gly	Ser	Gly	
316										20	25	30					
319	Arg	Tyr	Val	Trp	Ser	Asp	Gly	Cys	Thr	Tyr	Asp	Gly	Glu	Trp	Arg	Arg	
320										35	40	45					
323	Gly	Met	Arg	His	Gly	Gln	Gly	Lys	Thr	Met	Trp	Pro	Ser	Gly	Ala	Thr	
324										50	55	60					
327	Tyr	Glu	Gly	Glu	Tyr	Ser	Gly	Gly	Tyr	Ile	Tyr	Gly	Glu	Gly	Thr	Tyr	
328										65	70	75	80				
331	Thr	Gly	Ser	Asp	Asn	Ile	Val	Tyr	Lys								
332										85							
335	<210>	SEQ	ID	NO:	5												
336	<211>	LENGTH:	1227														
337	<212>	TYPE:	DNA														
338	<213>	ORGANISM:	Oryza sativa														
341	<220>	FEATURE:															
342	<221>	NAME/KEY:	CDS														
343	<222>	LOCATION:	(1)...(1227)														
345	<400>	SEQUENCE:	5														
346	cca	cgc	gtc	cg	aga	agc	ggc	cgc	ttt	ttt	ttt	ttg	ttt	tcc	cct	ccg	48
347	Pro	Arg	Val	Arg	Arg	Ser	Gly	Arg	Phe	Phe	Phe	Phe	Leu	Phe	Ser	Pro	Pro
348	1								5			10				15	
350	act	ccg	act	ccg	atc	gat	ctc	cac	ccc	gaa	tcc	ctc	ctc	acc	gcc		96
351	Thr	Pro	Thr	Pro	Ile	Asp	Leu	His	Pro	Glu	Ser	Leu	Leu	Leu	Thr	Ala	
352									20		25		30				
354	ggc	gag	ctt	ccg	gct	g	cg	g	ag	atg	gcc	aca	cgt	tat	tgg	atc	144
355	Gly	Glu	Leu	Pro	Ala	Ala	Ala	Glu	Met	Ala	Thr	Arg	Tyr	Trp	Ile	Val	
356									35		40		45				
358	tct	ctt	ccc	gtg	cag	act	cct	ggc	tcc	acc	gcc	aat	tct	ctc	tgg	g	192
359	Ser	Leu	Pro	Val	Gln	Thr	Pro	Gly	Ser	Thr	Ala	Asn	Ser	Leu	Trp	Ala	
360									50		55		60				
362	cgc	ctc	cag	gac	tcc	atc	tcg	cgc	cac	tcc	ttc	gac	acg	ccg	ctc	tac	240
363	Arg	Leu	Gln	Asp	Ser	Ile	Ser	Arg	His	Ser	Phe	Asp	Thr	Pro	Leu	Tyr	
364									65		70		75		80		
366	cgg	ttt	aa	c	gtc	ccc	gat	ctc	cg	gtc	ggc	acg	ctc	gac	tcc	ctc	288
367	Arg	Phe	Asn	Val	Pro	Asp	Leu	Arg	Val	Gly	Thr	Leu	Asp	Ser	Leu	Leu	
368									85		90		95				
370	gcc	ctc	agc	gac	gat	ctc	gtc	aag	tcc	aa	gtc	ttc	atc	gag	ggg	gtc	336
371	Ala	Leu	Ser	Asp	Asp	Leu	Val	Lys	Ser	Asn	Val	Phe	Ile	Glu	Gly	Val	

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:31; Xaa Pos. 23,56,57,104,126
Seq#:32; Xaa Pos. 23,56,57,104,126
Seq#:43; Xaa Pos. 64
Seq#:44; Xaa Pos. 64
Seq#:57; Xaa Pos. 34
Seq#:58; Xaa Pos. 34
Seq#:71; Xaa Pos. 956,961,1086
Seq#:72; Xaa Pos. 956,961,1086
Seq#:81; Xaa Pos. 264
Seq#:82; Xaa Pos. 264
Seq#:129; Xaa Pos. 226
Seq#:130; Xaa Pos. 226
Seq#:137; Xaa Pos. 2,6
Seq#:138; Xaa Pos. 2,6

VERIFICATION SUMMARY
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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:3062 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:31
L:3062 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:96
M:341 Repeated in SeqNo=31
L:3238 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:16
M:341 Repeated in SeqNo=32
L:4451 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:43
L:4451 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:192
L:4543 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:48
L:5699 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:57
L:5699 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:144
L:5947 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:32
L:8585 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:71
L:8585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71 after pos.:2880
M:341 Repeated in SeqNo=71
L:8923 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72 after pos.:944
M:341 Repeated in SeqNo=72
L:9867 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:81
L:9867 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81 after pos.:816
L:9979 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82 after pos.:256
L:14300 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:129
L:14300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:129 after pos.:720
L:14380 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:130 after pos.:224
L:14973 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:137
L:14973 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:137 after pos.:48
L:15270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:138 after pos.:0